## Multi-Gene Hereditary Cancer Testing among Men with Breast Cancer

## BACKGROUND

All men with a personal diagnosis of breast cancer are
candidates for $B R C A 1$ and $B R C A 2$ genetic testing beci pathogenic variants in these genes have a known association with breast cancer risk in both men and women. ${ }^{1}$
Additional genes with known breast cancer risk in women are now routinely included in multi-gene panel testing
Here, we evaluated the outcomes of multi-gene panel testing in a large cohort of men with breast cancer.

## METHODS

- This analysis includes 1,534 men with breast cancer who had testing with a multi-gene pan-cancer panel between
September 2013 and April 2017 .
genetic TESTING
- The multi-gene panel included BRCA1, BRCA2, ATM, CHEK2, PALB2, NBN, BARD1, PTEN, BRIP1, RAD51C RAD51D, MLH1, MSH2, EPCAM, MSH6, PMS2, APC, MUTYH, POLD1, POLE, GREM1, BMPR1A, SMAD4, TP53, STK11, CDH1, CDKN2A, and CDK
- All genes on the panel were available for the full time period starting in July 2016. starting in July 2016.
- Sequence and large rearrangement analysis was performed (sequencing only) and EPCAM, GREM1 (large rearrangement only).
- Pathogenic variants (PVs) are those that received a Deleterious.
ANALYSIS
- Clinical information was obtained from provider-completed test request forms.
- Personal cancer history and family cancer history were with PVs in other genes associated wit .
- The clinical presentation of men with PV , in genes with
no known association with breast cancer was assessed separately.

RESULTS
$231(15.1 \%)$ men with breast cancer were found to carry one or more PVs (Table 1).
PVs in BRCA2 (10.0\%) and CHEK2 (2.0\%) were most common.
7 men had a PV in two different genes, most commonly BRCA1/2 and CHEK2 ( $n=5$ ).

| Gene | Total PVs N (\%) | Prevalence | Second Breast Cancer |
| :---: | :---: | :---: | :---: |
| BRCA1 \& BRCA2 |  |  |  |
| BRCA2 | 153 (66.2\%) | 10.0\% | 3 |
| BRCA1 | 10 (4.3\%) | 0.7\% | $1+$ |
| Sub-total | 162 (70.1\%)* | 10.6\% | 4 |
| Other Breast Cancer-Risk Genes |  |  |  |
| CHEK2** | 30 (13.0\%) | 2.0\% | 2 |
| ATM | 14 (6.1\%) | 0.9\% | $2^{+}$ |
| PALB2 | 14 (6.1\%) | 0.9\% | 0 |
| NBN | 5 (2.2\%) | 0.3\% | 0 |
| BARD1 | 4 (1.7\%) | 0.3\% | 1 |
| CDH1 | 1 (0.4\%) | <0.1\% | 1 |
| TP53 | 1 (0.4\%) | <0.1\% | 0 |
| Sub-total | 69 (29.9\%) | 4.5\% | 6 |
| Lynch Syndrome Genes |  |  |  |
| MSH6 | 2 (0.9\%) | 0.1\% | 0 |
| MLH1 | 1 (0.4\%) | <0.1\% | 0 |
| PMS2 | 1 (0.4\%) | <0.1\% | 0 |
| Sub-total | 4 (1.7\%) | 0.3\% | 0 |
| Other Cancer-Risk Genes |  |  |  |
| BRIP1 | 1 (0.4\%) | <0.1\% | 0 |
| CDKN2A | 1 (0.4\%) | <0.1\% | 0 |
| Sub-total | 2 (0.9\%) | 0.1\% | 0 |
| Total | 231* | 15.1\% | $9(3.9 \%)^{+}$ |
| ${ }^{*} 7$ men had PVs in two different genes (BRCA2 and CHEK2, 4; BRCA1 and CHEK2, 1; BRCA1 and ATM, 1; BRCA1 and BRCA2, 1) <br> *233/30 (76.7\%) PVs in CHEK2 were c.1100del <br> ${ }^{\dagger 1}$ man with PVs in both BRCA1 and ATM had a second breast cancer |  |  |  |

There were no substantial differences in the median age-at-diagnosis for men without a PV (66) compared to
those with a PV in BRCA1/2 (66) or a PV in another gene (63)

- Fewer men with a PV in BRCA1/2 had a second breast cancer relative to men with a PV in another breast cancer risk gene ( $1.9 \%$ versus $7.9 \%$; Figure 1 ).
A personal and/or family history of prostate, pancreatic, female breast, and ovarian cancer was more commo among men with a PV in BRCA1/2 compared to men with a PV in another breast cancer risk gene (Figure 1).

This is consistent with the penetrance and cancer spectrum of BRCA $1 / 2$ relative to the other breast cancer genes.


- A personal and family history of colon cancer was reported for Lynch syndrome (Table 2).
One man with a PV in MSH6 was diagnosed with breast cancer at age 39 and reported no other personal or family cancer history (Table 2).

Table 2. Personal and Family Cancer History for Men with PVs in Genes with No Known Breast Cancer Risk

| Gene | $\begin{aligned} & \text { Personal History } \\ & \text { (Age at Dx) } \end{aligned}$ | Family History (Age at Dx) |
| :---: | :---: | :---: |
| MLH1 | Breast (65) Colon (36) Duodenum (61) Melanoma (62) | FDR: Colon $(23,43,48)$ and Ovarian (46); FDR: Colon (75); FDR: Rectum (62) |
| MSH6 | Breast (62) Other (75) | FDR: Breast (63); SDR: Gastric (70); SDR: Pancreas (70) |
| MSH6 | Breast (39) | None |
| PMS2 | Breast (79) | None |
| BRIP1 | Breast (65) | FDR: Colon (67) |
| CDKN2A | Breast (70) | FDR: Breast (age unknown); SDR: Breast (age unknown) |

## CONCLUSIONS

- Nearly one third of all PVs identified in men with breast
cancer here were in a gene other than BRCA1 or BRCA2.
- PVs were identified in several genes with no known breast cancer risk, very few of which were predicted by additiona
personal and family cancer history
- There were no obvious differences in the clinical presentation
of men with PVs in BRCA1 or BRCA2 compared to men with of men with PVs in BRCA1 or BRCA2 compared to men with
PVs in most of the other panel genes, which suggests that multi-gene panel testing may be appropriate for all men with breast cancer regardless of other personal or family history.

REFERENCES

1. Daly M, Piarski R, Berry M, etal. Genentic/Familial High-Risk Assessment: Breas
